

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION
<120> Receptor proteins specifically recognizing bacterial DNA
<130> A031-29PCT
<140> <141>
<150> 2000-219652 <151> 2000-07-19
<160> 5
<170≻ PatentIn Ver. 2.1
<pre><210> 1 <211> 3257 <212> DNA <213> Homo sapiens</pre>
<220> <221> CDS <222> (107) (3205)
<pre><400> 1 ccgctgctgc ccctgtggga agggacctcg agtgtgaagc atccttccct gtagctgctg 60</pre>
tocagicigo cogocagaco ciciggagaa gococigoco cocago aig ggi tio 115 Met Gly Phe I
tgc cgc agc gcc ctg cac ccg ctg tct ctc ctg gtg cag gcc atc atg 163 Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln Ala Ile Met 5 10 15
ctg gcc alg acc ctg gcc ctg ggt acc ttg cct gcc ttc cta ccc tgt Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys 20 25 30 35
gag ctc cag gcc cac ggc ctg gtg aac tgc aac tgg ctg ttc ctg aag 259 Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe Leu Lys 40 45 50

		t c c Se r						307
		aac Asn						355
		ctg Leu						403
		ccc Pro 105						451
		gct Ala						499
		ac t Thr						547
		acc Thr						595
		ctg Leu						643
		agg Arg 185						691
		ctc Leu						739
		aac Asn						787
		gtc Val						835

240

		ctc Leu							883
		tgc Cys 265							931
		agc Ser							979
		tcc Ser							1027
		ctg Leu							1075
		gcc Ala							1123
		tac Tyr 345							1171
		ggg Gly							1219
		cgc Arg		-		_			1267
		ctc Leu							1315
		ggc Gly							1363

235

230

					tcg Ser			1411
					tgg Trp			1459
					tct Ser			1507
					ctg Leu			1555
					ctc Leu 495			1603
					gca Ala			1651
					gac Asp			1699
					gag Glu			1747
					ttt Phe			1795
					cgc Arg 575			1843
					gtg Val			1891
					ggc Gly			1939

Y

			600				605			610		
_	tgg Trp	-			-		-				-	1987
	ttg Leu 630											2035
	caa Gln											2083
	gac Asp			-	-		_	 				2131
	aaa Lys											2179
	aat Asn											2227
	tgc Cys 710											2275
	gag Glu											2323
	cac His											2371
	agc Ser											2419
	ctg Leu											2467

								agc Ser 800			2515
								tgg Trp			2563
Α								gtg Val			2611
								cac His			2659
								gat Asp			2707
								cag Gln 880			2755
-	_	 -		-		 _	_	gag Glu	 _	_	2803
G								gac Asp			2851
								tat Tyr			2899
								agt Ser			2947
								gag Glu 960			2995
								cgc Arg			3043

3235

3257

965 970 975 tac gig egg eig ege eag ege ete ige ege eag agi gie eie eie igg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp 990 ccc cac cag ccc agt ggt cag cgc agc tic tgg gcc cag ctg ggc atg Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met 1000 1010 gcc cig acc agg gac aac cac cac tic tat aac cgg aac tic igc cag Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln 1015 1020 gga ccc acg gcc gaa tag ccgtgagccg gaatcctgca cggtgccacc Gly Pro Thr Ala Glu 1030 tecacactea ceteacetet ge <210> 2 <211> 1032 <212> PRT <213> Homo sapiens <400> 2 Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln 5 10 Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe 25 Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu 40 Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn 55 Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp 70 75 Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp 85 90 Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met 105 Thr lie Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu 120

140

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser 135

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser

```
145
                  150
                                     155
Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
                                  170
               165
Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
                              185
Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
                          200
Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
                       215
Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
                   230
                                      235
Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
                                  250
               245
Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
                              265
Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
                          280
Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
                      295
                                          300
Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu
                  310
                                      315
Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
               325
                                  330
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
                              345
His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
                           360
Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
                      375
Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
                   390
                                      395
Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
                                  410
Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu
           420
                              425
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu
                          440
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu
                      455
Asp Phe Arg Pro Asn Cvs Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser
                  470
                                      475
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
              485
                                  490
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val
                              505
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu
```

												-0-			
_		515					520					525		٠.	
Ser	His	Asn	Lys	Leu	Asp		Tyr	His	Glu	His		Phe	Thr	Glu	Leu
	530					535					540				
Pro	Arg	Leu	Glu	Ala		Asp	Leu	Ser	Tyr		Ser	Gln	Pro	Phe	
545					550					555					560
Met	Gln	Gly	Val	Gly	His	Asn	Phe	Ser	Phe	Val	Ala	His	Leu	Arg	Thr
				565					570					575	
Leu	Arg	His	1.eu	Ser	Leu	Ala	His	Asn	Asn	He	His	Ser	Gln	Val	Ser
			580					585					590		
Gl n	Gln	Lau		Ser	Thr	Sor	Lou		Δla	Lon	Δen	Phe		Glv	Aen
orn	0111	595	Cys	JUI	1111	561	600	MIS	лια	LCu	пор	605	501	Ory	лэп
	T			W-1	т	41-		C1	۸	1	т		п: -	nt -	DL -
Ala	Leu	GIY	HIS	мет	rp		GIU	GIY	ASP	Leu		Leu	HIS	rne	rne
	610				_	615	_	_		_	620				_
Gln	Gly	Leu	Ser	Gly	Leu	He	Trp	Leu	Asp		Ser	Gln	Asn	Arg	
625					630					635					640
His	Thr	Leu	Leu	Pro	Gln	Thr	Leu	Arg	Asn	Leu	Pro	Lys	Ser	Leu	Gln
				645					650					655	
Val	Leu	Arg	Leu	Arg	Asp	Asn	Tyr	Leu	Ala	Phe	Phe	Lys	Trp	Trp	Ser
			660					665					670		
Leu	His	Phe	Leu	Pro	Lvs	Leu	Glu	Val	Leu	Asp	Leu	Ala	Glv	Asn	Gln
D.O.		675			-,-		680					685	,		
Lan	Lvs		Lan	The	Acn	Clv		Lou	Dro	A 1 a	Clv		Δια	Lau	Λισ
Leu	690	Αια	LCu	1111	лэн	695	361	Ltu	110	лια	700	1111	мв	LCu	AI 6
			17 - 1	c	C		c		c	DL -		41-	D	C1	DL -
-	Leu	ASD	vai	ser	-	ASI	ser	116	ser		vai	ATA	110	GIY	
705					710				_	715	_	_			720
Phe	Ser	Lys	Ala		Glu	Leu	Arg	Glu		Asn	Leu	Ser	Ala		Ala
				725					730					735	
Leu	Lys	Thr	Vai	Asp	His	Ser	Trp	Phe	Gly	Pro	Leu	Ala	Ser	Ala	Leu
			740					745					750		
Gln	He	Leu	Asp	Val	Ser	Ala	Asn	Pro	Leu	His	Cys	Ala	Cys	Gly	Ala
		755					760					765			
Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	Val	Gln	Ala	Ala	Val	Pro	Glv	Leu
	770					775					780			•	
Pro	Ser	Δισ	Val	Ive	Cvs		Ser	Pro	Glv	Gln		Gin	Glv	Len	Ser
785	oci	1118		L,3	790	01,	50.	110	01,	795	Dea	0111	01,	Deu	800
	Phe	410	CID	Ann		A = c	Lou	Cvo	Lou		Clu	A10	Lou	co.	
116	rne	Ald	GIII	805	Leu	AIB	Leu	Cys	810	АЗР	UIU	Ald	Leu	815	пр
	0	Di.			0	T		41.		41-	I	C1	1		W-1
Asp	Cys	Phe		Leu	Ser	Leu	Leu		vaı	Ala	Leu	GIY		GIY	vai
			820					825					830		
Pro	Met	Leu	His	His	Leu	Cys	Gly	Тгр	Asp	Leu	Trp	Туг	Cys	Phe	His
		835					840					845			
Leu	Cys	Leu	Ala	Trp	Leu	Pro	Тгр	Arg	Gly	Arg	Gin	Ser	Gly	Arg	Asp
	850					855					860				
Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	Phe	Val	Val	Phe	Asp	Lys	Thr	Gln
865					870					875			-		880
	Ala	Val	Ala	Asn		Val	Tvr	Asn	Glu		Arg	Glv	Gln	Leu	
201								1			0				

885 890 Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp 905 Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr 920 Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser 935 940 Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu 950 955 Asp Arg Lys Asp Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg 965 970 Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val 985 980 Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln 1000 1005 Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn 1015 1020 Phe Cvs Gln Glv Pro Thr Ala Glu 1025 1030

<210> 3

<211> 3471

<212> DNA <213> Mus musculus

<220>

<221> CDS

<222> (107).. (3205)

<400> 3

tgaaagtgtc acticctcaa tictcigaga gaccciggtg tggaacatca tictcigccg 60

- cccagiligi cagagggagc clcgggagaa icclccaict cccaac aig gil cic 115 Mei Val Leu
- egt ega agg act etg eac ecc tig lec etc etg gla eag get gea gig 163 Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gin Ala Ala Val 5 10
- ctg get gag act ctg gec ctg ggt acc ctg cet gec ite cta cec tgt 211 Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys 20 25 30 35



			ggc Gly						259
			tct Ser						307
			aac Asn						355
			ctg Leu						403
			ccc Pro 105						451
			gct Ala						499
			ac t Thr						547
			acc Thr						595
			ctg Leu						643
			aca Thr 185						691
			ctc Leu						739
			caa Gln						787



215 220 225

tat Tyr								835
tcc Ser 245								883
gcc Ala								931
cct Pro								979
gac Asp								1027
aac Asn								1075
aac Asn 325								1123
ctg Leu								1171
gca Ala								1219
ggc Gly								1267
ga t Asp								1315



						ctt Leu		1363
						ctg Leu		1411
						ctg Leu		1459
						aag Lys 465		1507
						tct Ser		1555
						tca Ser		1603
						gtc Val		1651
						ctg Leu		1699
						cta Leu 545		1747
						agc Ser		1795
						atg Met		1843
						tcc Ser		1891

580		585	590)	595
		Val Arg Phe		e agc ggc aac e Ser Gly Asn	
				c cat ttc ttc i His Phe Phe 625	
Leu Ser G			Leu Ser Gli	a aat aac ctg n Asn Asn Leu 640	
	-	-		g agc ctg aag s Ser Leu Lys 655	
				tgg acc agt Trp Thr Ser	
				a ggc aac cag a Gly Asn Gln	_
				ctc ctc cag Leu Leu Gin 705	
Asp Val S			Ser Val Val	c cca gcc ttc Pro Ala Phe 720	
				cac aac att His Asn Ile 735	
				g atg aac ctg Met Asn Leu ' 	
				tgt ggg gca a Cys Gly Ala	

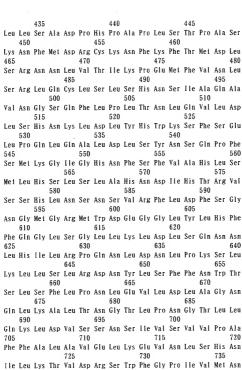


	gac Asp								2467
	gtg Val								2515
	cag Gln 805								2563
	ggc Gly								2611
	cac His								2659
	gca Ala								2707
	ccc Pro								2755
	gac Asp 885								2803
	cgc Arg								2851
	cag Gln								2899
	act Thr								2947
cgc									

950	955	960
gac gig gig gig tig gig atc Asp Val Val Leu Val IIe 965 970	Leu Arg Pro Asp Ala	
tat gtg cga ctg cgc cag cgt Tyr Val Arg Leu Arg Gln Arg 980 985		
ccc cag cag ccc aac ggg cag Pro Gln Gln Pro Asn Gly Gln 1000		
gcc cig act agg gac aac cgc Ala Leu Thr Arg Asp Asn Arg 1015		
gga cct aca gca gaa tag ctc Gly Pro Thr Ala Glu 1030	agagcaa cagciggaaa ca	agetgeate 3235
ticatgeetg gitecegagi igete	tgcct gccttgctct gtc	ttactac accgctattt 3295
ggcaagtgcg caatatatgc tacca	ageca ccaggeceae ggas	gcaaagg tiggcagtaa 3355
agggtagttt tcttcccatg catct	ticag gagagigaag ata	gacacca gacccacaca 3415
gaacaggact ggagttcatt ctctg	ccct ccaccccact tigo	ectgtet etgtat 3471
<210> 4 <211> 1032 <212> PRT <213> Mus musculus		
<400> 4	tou His Day Lou Con	Lau Lau Val Cla
Met Val Leu Arg Arg Arg Thr 1 5	10	15
Ala Ala Val Leu Ala Glu Thr 20	Leu Ala Leu Gly Thr 25	Leu Pro Ala Phe 30
Leu Pro Cys Glu Leu Lys Pro 35	His Gly Leu Val Asp 40	Cys Asn Trp Leu 45
Phe Leu Lys Ser Val Pro Arg	Phe Ser Ala Ala Ala	Ser Cys Ser Asn
Ile Thr Arg Leu Ser Leu Ile		His Leu His Asn



65 75 70 Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp 90 85 Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met 105 Thr lle Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu 120 Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser 135 140 Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala 150 155 Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly 165 170 Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro 185 Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Val Lys Tyr 195 200 Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr 215 Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu 230 235 Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg 245 250 Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser 265 Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly 280 Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe 295 300 Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu 310 315 Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu 330 325 Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala 345 Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu 360 Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu 380 375 Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met 390 395 Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala 410 Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr 425 Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu



745 740 Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly 760 Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly 775 780 Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg 790 795 Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser



810 Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val 825 Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe 840 His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser 855 Ala Gin Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gin 870 875 Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu 890 Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp 905 Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr 920 Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser 935 940 Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu 950 955 Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His 965 970 Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val 985 Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln 1005 1000 Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn 1015 1020 Phe Cys Arg Gly Pro Thr Ala Glu 1030

<210> 5 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CpG ODN

<400> 5

tccatgacgt tcctgatgct

20